Harris, A.
09/285292

-key terms

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     FILE 'REGISTRY' ENTERED AT 14:33:58 ON 01 FEB 2005
                E "25-HYDROXYVITAMIN D3 24-HYDROLASE"/CN 5
L1             2 S "25-HYDROXYVITAMIN D3 24-HYDROXYLASE"?/CN

     FILE 'CAPLUS' ENTERED AT 14:34:27 ON 01 FEB 2005
L1             2 SEA FILE=REGISTRY ABB=ON  PLU=ON  "25-HYDROXYVITAMIN D3
                  24-HYDROXYLASE"?/CN
L4           362 SEA FILE=CAPLUS ABB=ON  PLU=ON  (L1 OR 25(W)(HYDROXYVITAMIN OR
                  HYDROXY VITAMIN)(4W)HYDROXYLASE OR CYP24 OR CYP 24 OR GENBANK(S
                  )(U60669 OR U 60669 OR S78775 OR "S 78775")) AND (DETERM? OR
                  DETECT? OR DET## OR SCREEN? OR MEAS? OR QUANT?)
L5            39 SEA FILE=CAPLUS ABB=ON  PLU=ON  L4 AND (HYBRIDIS? OR HYBRIDIZ?
                  OR CGH OR AMPLIF?)
L7            17 SEA FILE=CAPLUS ABB=ON  PLU=ON  L5 AND (CANCER? OR CARCIN? OR
                  TUMOUR OR TUMOR OR NEOPLAS?)

L7   ANSWER 1 OF 17  CAPLUS  COPYRIGHT 2005 ACS on STN
ED   Entered STN:  17 Dec 2004
ACCESSION NUMBER:          2004:1081026  CAPLUS
DOCUMENT NUMBER:           142:50129
TITLE:                     Microarray for determining expression of
                           psychoneuroendocrinimmune genes and diagnosis of
                           diseases
INVENTOR(S):               Nicholson, Ainsley; Vernon, Suzanne D.
PATENT ASSIGNEE(S):        The Government of the United States as Represented by
                           the Secretary of the Department of Health and Human
                           Services, USA
SOURCE:                    PCT Int. Appl., 254 pp.
                           CODEN: PIXXD2
DOCUMENT TYPE:             Patent
LANGUAGE:                  English
FAMILY ACC. NUM. COUNT:    1
PATENT INFORMATION:

     PATENT NO.            KIND   DATE        APPLICATION NO.          DATE
     ----------------      ----   --------    ---------------------    --------
     WO 2004108899          A2    20041216    WO 2004-US17686          20040604
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI,
             NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,
             TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK,
             EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE,
             SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
             SN, TD, TG
PRIORITY APPLN. INFO.:                         US 2003-475915P     P  20030604
AB   Disclosed are compns. and methods for microarrays comprising genes
     involved in psychoneuroendocrinimmune (PNI) activity. An oligonucleotide
     microarray composed entirely of PNI genes was designed, which can allow a
     researcher to assess the overall psychoneuroendocrineimmune state of an
     individual, and to observe systemic responses to various stresses. The
     PNI array has widespread applicability and marketability in the diagnosis
     and treatment of diseases that result from dysregulation of the
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hypothalamic-pituitary-adrenal axis. A total of 1451 genes encoding 1738 transcriptional products can be distinguished and samples from human or mouse can **hybridize** with equal affinity, facilitating animal studies. Arabidopsis and housekeeping genes are used as controls. To **determine** the extent of peripheral blood PNI gene expression, both EST and microarray databases were queried; there were 566 genes from an EST database that matched to one of 1622 genes in the PNI database. The utility of the PNI array is demonstrated for research of chronic fatigue syndrome and other diseases involving PNI.

L7 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 29 Jun 2004
ACCESSION NUMBER: 2004:522188 CAPLUS
DOCUMENT NUMBER: 141:171860
TITLE: No evidence for **amplification** of 25-hydroxyvitamin D-1α-OHase (1α-OHase) or 1,25-dihydroxyvitamin D-24-OHase (24-OHase) genes in malignant melanoma (MM)
AUTHOR(S): Reichrath, Jorg; Rafi, Leyla; Rech, Martin; Meineke, Viktor; Tilgen, Wolfgang; Seifert, Markus
CORPORATE SOURCE: Department of Dermatology, Kirrberger Str., The Saarland University Hospital, Homburg/Saar, 66421, Germany
SOURCE: Journal of Steroid Biochemistry and Molecular Biology (2004), 89-90(1-5), 163-166
CODEN: JSBBEZ; ISSN: 0960-0760
PUBLISHER: : Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Increasing evidence points at an important function of Vitamin D metabolites for growth regulation in various tissues, including MM. Using array **CGH, amplification** of 24-OHase was recently **detected** as a likely target oncogene of the **amplification** unit 20q13.2 in breast **cancer** cell lines and **tumors**. Addnl., **amplification** of 1α-OHase has been reported in human malignant glioma. Using immunohistochem., the authors have now **detected** nuclear Vitamin D receptor (VDR) immunoreactivity in primary cutaneous malignant melanoma (MM), indicating that Vitamin D metabolites may be of importance for the growth regulation in these **tumors**. Using Southern anal., the authors have analyzed MM and metastases for evidence of **amplification** of 1α-OHase or 24-OHase genes. The authors' results do not support the hypothesis that **amplification** of 1α-OHase or 24-OHase genes may be of importance for pathogenesis or progression of MM.
REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Oct 2003
ACCESSION NUMBER: 2003:799401 CAPLUS
DOCUMENT NUMBER: 140:39712
TITLE: **Determination** of amplicon boundaries at 20q13.2 in tissue samples of human gastric adenocarcinomas by high-resolution microarray comparative genomic **hybridization**
AUTHOR(S): Weiss, Marjan M.; Snijders, Antoine M.; Kuipers, Ernst

J.; Ylstra, Bauke; Pinkel, Daniel; Meuwissen, Stefan G. M.; van Diest, Paul J.; Albertson, Donna G.; Meijer, Gerrit A.
CORPORATE SOURCE: Department of Gastroenterology, VU University Medical Centre, Amsterdam, Neth.
SOURCE: Journal of Pathology (2003), 200(3), 320-326
CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Comparative genomic **hybridization** (**CGH**) of gastric adenocarcinomas frequently shows gains and **amplifications** of chromosome 20. However, the underlying genetic lesion is unknown and conventional **CGH** results do not allow specification of the target region. In order to investigate this chromosomal aberration with a higher resolution and sensitivity, microarray-based **CGH** was performed with both scanning and high-resolution arrays of chromosome 20 in a series of 27 gastric adenocarcinomas. Locus-specific fragments of genomic DNA from bacterial artificial chromosome (BAC) clones were spotted as microarrays. A scanning array contained a set of 27 BAC clones covering chromosome 20q. A high-resolution array contained 27 overlapping BAC clones at 20q13.2. This high-resolution array was used to narrow down the amplicon at 20q13.2 in **tumors** showing **amplification** of this chromosomal region with the scanning array. Pos. copy number changes on chromosome 20q were **detected** in 12 of 27 cases (44%). These changes included gain of the whole arm of chromosome 20q in 8 of 27 (30%) cases, **amplification** restricted to 20q12.1 in one case, and **amplifications** restricted to 20q13 in three cases (11%). The three **tumors** showing **amplification** restricted to 20q13 were analyzed further using the high-resolution array. In one **tumor**, the whole contig was **amplified** at a constant level. One of the other two **tumors** had a clear proximal breakpoint, while the other **tumor** had a clear distal breakpoint within the 20q13.2 region. The proximal and the distal breakpoint were approx. 800 kb apart. In the present study, an amplicon at 20q13.2 has been narrowed down to 800 kb which is likely to harbor one or more putative oncogenes relevant to gastric **carcinogenesis**, for which ZNF217 and **CYP24** are good candidates.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 24 Sep 2003
ACCESSION NUMBER: 2003:748376 CAPLUS
DOCUMENT NUMBER: 140:88060
TITLE: Combination of vitamin D metabolites with selective inhibitors of vitamin D metabolism
AUTHOR(S): Schuster, Inge; Egger, Helmut; Herzig, Gerda; Reddy, G. Satyanarayana; Vorisek, Georg
CORPORATE SOURCE: Institute of Pharmaceutical Chemistry, University Vienna, Vienna, 1090, Austria
SOURCE: Recent Results in Cancer Research (2003), 164(Vitamin D Analogs in Cancer Prevention and Therapy), 169-188
CODEN: RRCRBU; ISSN: 0080-0015
PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal
LANGUAGE: English
AB 1α,25(OH)2D3 exerts antiproliferative, differentiating effects on many cell types, including **cancer** tissues. In most of its target cells, levels of 1α,25(OH)2D3 are regulated by local synthesis via CYP27B and metabolism via **CYP24**. Rapidly induced by vitamin D, **CYP24** repeatedly hydroxylates the vitamin D side chain and ultimately terminates hormonal activity. Aiming at increased hormone levels, lifetime and function, numerous vitamin D analogs were synthesized with structural modifications, which impede oxidation of the vitamin D side chain. The authors' group followed a different strategy, namely, blocking 1,25(OH)2D3 metabolism with inhibitors of **CYP24**. As appropriate inhibitors, the authors exploited compds. termed azoles, which directly bind to the heme iron of the CYPs via an azole nitrogen and to other parts of the substrate site. The authors synthesized some 400 azoles and tested their potential to selectively inhibit **CYP24**, but not hormone synthesis by the related CYP27B. Using primary human keratinocyte cultures as the source of **CYP24** and CYP27, the authors discovered some 50 inhibitors of **CYP24** with IC50 values in the nanomole range and selectivities up to 60-fold. As the first representative of selective **CYP24** inhibitors, VID400 underwent preclin. development. In human keratinocytes, VID400 stabilized levels of endogenously produced 1α,25(OH)2D3, and thereby strongly **amplified** and prolonged expression of **CYP24**, a surrogate marker of hormonal function. In parallel, antiproliferative activity showed up at 100-fold or more lower concns. of 1α,25(OH)2D3. This data suggests that **CYP24** inhibitors could become attractive drugs in antiproliferative therapy, used as single entities to increase or extend endogenous hormone function or in combination with low doses of potent analogs. Moreover, the authors used selective inhibitors as valuable tools to (a) elucidate regulatory mechanisms of vitamin D synthesis and metabolism, (b) **determine** intrinsic activities of the otherwise highly, transient vitamin D metabolites and (c) model the active sites of **CYP24** and CYP27B.
REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 14 Feb 2003
ACCESSION NUMBER: 2003:117965 CAPLUS
DOCUMENT NUMBER: 138:164855
TITLE: Polymorphisms in mammalian STK15 (STK6) genes encoding kinases associated with susceptibility for **cancer** and methods for diagnosis and therapy
INVENTOR(S): Toland, Amanda E.; Balmain, Allan
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 92 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003012046	A2	20030213	WO 2002-US24115	20020729

WO 2003012046 A3 20030828
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2003108910 A1 20030612 US 2002-209324 20020729
PRIORITY APPLN. INFO.: US 2001-308911P P 20010727
US 2001-334146P P 20011128

AB The present invention provides methods for **determining cancer** susceptibility in a human subject by identifying a single nucleotide polymorphism (SNP) of the STK15 gene of human resulting in STK15 kinase Ile31 mutation as well as mouse STK6 gene polymorphisms associated with **cancer**. The invention provides methods and kits for identifying agents that affect **tumor** susceptibility. Furthermore, the invention provides methods for **detecting** low penetrance **tumor** susceptibility genes. Linkage and haplotype anal. using mouse skin model system and association studies with human breast **cancer** populations provided evidence for germline polymorphisms on distal mouse chromosome 2/human chromosome 20q13 that confer increased **cancer** risk.

L7 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 04 Oct 2002
ACCESSION NUMBER: 2002:754553 CAPLUS
DOCUMENT NUMBER: 137:227626
TITLE: Methods for diagnosing and monitoring malignancies by **screening** gene copy numbers
INVENTOR(S): Kuo, Wen-Lin; Polikoff, Daniel; Pinkel, Daniel; Albertson, Donna; Berchuk, Andy; Gray, Joe W.
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077197	A2	20021003	WO 2002-US9419	20020327
WO 2002077197	A3	20031023		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA,

GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2003077582 A1 20030424 US 2001-819148 20010327
PRIORITY APPLN. INFO.: US 2001-819148 A 20010327
AB The invention concerns the discovery that an **amplification** of some genes or an increase in that gene activity and a deletion of some genes or a decrease in that gene activity is a marker for the presence of, progression of, or predisposition to, a **cancer** (e.g., breast **cancer**). Using this information, this invention provides methods of **detecting** a predisposition to **cancer** in an animal. The methods involve (i) providing a biol. sample from an animal (e.g. a human patient); (ii) **detecting** the level of the genes of the present invention within the biol. sample; and (iii) comparing the level of one or more of said genes with a level of one or more of said genes in a control sample taken from a normal, **cancer**-free tissue.

L7 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 06 Sep 2002
ACCESSION NUMBER: 2002:671255 CAPLUS
DOCUMENT NUMBER: 138:247879
TITLE: Analysis of 1C-gene array for toxic response using RNA isolated from HepG2 cells treated with anticancer drugs
AUTHOR(S): Hong, Yulong; Bao, Paul; Xie, Xinying; Mooney, Jeffrey L.; Mueller, Uwe R.; Lai, Fang
CORPORATE SOURCE: Corning Inc., Corning, NY, USA
SOURCE: Proceedings of SPIE-The International Society for Optical Engineering (2002), 4626(Biomedical Nanotechnology Architectures and Applications), 23-34
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The possibility of using microarray technol. for mechanistic understanding of drug toxicity has opened up a new research field in toxicol. In an attempt to build knowledge in the field, we have designed a 1C-gene array composed of 85 known human genes with toxicol. interests and 15 control genes. HepG2 cells were treated with ethanol and two anticancer drugs, mitomycin C and doxorubicin. RNA were isolated and labeled by fluorescent dyes, then **hybridized** to the 1C-gene array. Our results showed that a number of cytochrome P 450 genes, such as CYP4F2/3, CYP3A3, **CYP24**, and CYP51, were consistently responsive to the toxicant treatment. However, different genes responded to different toxicants. For example, **CYP24** and CYP51 were up-regulated by the ethanol treatment but remained unresponsive to the other two drugs. The anticancer drugs, but not ethanol differentially regulated several other genes including CYP3A3, TNFRSF6 and CHES1, implying that the two drugs might function through a similar mechanism, which differs from that of ethanol. The reproducibility of our results suggests that microarray-based expression anal. may offer a rapid and efficient means of assessing drug toxicity.
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 28 Mar 2002
ACCESSION NUMBER: 2002:241013 CAPLUS

DOCUMENT NUMBER: 136:277466
TITLE: Expressed gene sets as markers for specific tumors
INVENTOR(S): Ramaswamy, Sridhar; Golub, Todd B.; Tamayo, Pablo; Angelo, Michael
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Dana-Farber Cancer Institute, Inc.
SOURCE: PCT Int. Appl., 715 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002024956	A2	20020328	WO 2001-US29287	20010919
WO 2002024956	C1	20030306		
WO 2002024956	A3	20030626		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2002024956	A2	20020328	WO 2001-XA29287	20010919

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

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WO 2002024956	A2	20020328	WO 2001-XB29287	20010919

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

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WO 2002024956	A2	20020328	WO 2001-XC29287	20010919

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,

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AU 2001092802	A5	20020402	AU 2001-92802	20010919
US 2002110820	A1	20020815	US 2001-955920	20010919
EP 1339872	A2	20030903	EP 2001-973197	20010919
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2004509629	T2	20040402	JP 2002-529548	20010919
PRIORITY APPLN. INFO.:			US 2000-233534P	P 20000919
			US 2001-278749P	P 20010326
			WO 2001-US29287	W 20010919

AB Sets of genetic markers for specific tumor classes are described, as well as methods of identifying a biol. sample based on these markers. Total RNA was isolated from .apprx.300 human tumor and normal tissue specimens representing 30 individual classes of tumor or normal tissue, and cDNA produced using established mol. biol. protocols was hybridized to two high d. Affymetrix oligonucleotide microarrays (Hu6800FL and Hu35KsubA0). Raw expression data was combined into a master data set containing the expression values for between 6800 and 16,000 genes expressed by each individual sample. A filter was applied to this data set which only allows those genes expressed at 3-fold above baseline and with an absolute difference in expression value of 100 to pass. By comparing the sets of genes which are expressed specifically in one class of tumor (e.g., pancreatic adenocarcinoma) vs. its accompanying normal tissue (e.g., normal pancreas), sets of genes were determined which are specific to various tumors and their normal tissue counterparts. Also described are diagnostic, prognostic, and therapeutic screening uses for these markers, as well as oligonucleotide arrays comprising these markers. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L7 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 19 Oct 2001
ACCESSION NUMBER: 2001:763251 CAPLUS
DOCUMENT NUMBER: 135:299597
TITLE: Genes differentially expressed in human foam cell differentiation
INVENTOR(S): Shiffman, Dov; Somogyi, Roland; Lawn, Richard; Seilhamer, Jeffrey J.; Porter, Gordon J.; Mikita, Thomas; Tai, Julie
PATENT ASSIGNEE(S): Incyte Genomics, Inc., USA
SOURCE: PCT Int. Appl., 315 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001077389	A2	20011018	WO 2001-US11128	20010404
WO 2001077389	A3	20030424		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				

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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2403946	AA	20011018	CA 2001-2403946	20010404
EP 1358347	A2	20031105	EP 2001-924723	20010404
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
JP 2004532602	T2	20041028	JP 2001-575243	20010404
US 2003165924	A1	20030904	US 2002-240965	20021004
PRIORITY APPLN. INFO.:			US 2000-195106P P	20000405
			WO 2001-US11128 W	20010404

AB The present invention relates to 276 purified polynucleotides and compns. comprising pluralities of polynucleotides that are differentially expressed during human foam cell development and are associated with atherosclerosis. The present invention presents the use of the compns. as elements immobilized on a substrate for **hybridization**, and provides methods for using the compns. and polynucleotides in the diagnosis of conditions, disorders, and diseases associated with atherosclerosis.

L7 ANSWER 10 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 28 Jun 2001
ACCESSION NUMBER: 2001:464581 CAPLUS
DOCUMENT NUMBER: 136:113565
TITLE: A **quantitative** trait locus influencing estrogen levels maps to a region homologous to human chromosome 20
AUTHOR(S): Martin, Lisa J.; Blangero, John; Rogers, Jeffrey; Mahaney, Michael C.; Hixson, James E.; Carey, K. Dee; Morin, Phillip A.; Comuzzie, Anthony G.
CORPORATE SOURCE: Departments of Genetics and Physiology and Medicine, Southwest Foundation for Biomedical Research San Antonio, TX, 78245-0549, USA
SOURCE: Physiological Genomics [online computer file] (2001), 5(2), 75-80
CODEN: PHGEFP; ISSN: 1094-8341
URL: http://physiolgenomics.physiology.org/cgi/reprint/5/2/75
PUBLISHER: American Physiological Society
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB Estrogen, a steroid hormone, regulates reproduction and has been implicated in several diseases. We performed a genome-wide scan using multipoint linkage anal. implemented in a general pedigree-based variance component approach to identify genes with **measurable** effects on variation in estrogen levels in baboons. A microsatellite polymorphism, D20S171, located on human chromosome 20q13.11, showed strong evidence of linkage with aLOD score of 3.06 (P = 0.00009). This region contains several potential candidate genes including melanocortin 3 receptor(MC3R),

cytochrome P 450 subfamily XXIV (**CYP24**), and breast **carcinoma amplified** sequence (BCAS1). This is the first evidence of a **quant.** trait locus with a significant effect on estrogen.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 01 Jun 2001
ACCESSION NUMBER: 2001:397090 CAPLUS
DOCUMENT NUMBER: 135:15154
TITLE: Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for **detection** thereof
INVENTOR(S): Cargill, Michele; Ireland, James S.; Lander, Eric S.
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA
SOURCE: PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001038576	A2	20010531	WO 2000-US31639	20001117
WO 2001038576	A3	20020711		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-167334P P 19991124

AB The invention provides nucleic acid segments of the human genome, particularly nucleic acid segments from the coding region of a gene, including polymorphic sites. Allele-specific primers and probes **hybridizing** to regions flanking or containing these sites are also provided. The nucleic acids, primers and probes are used in applications such as phenotype correlations, forensics, paternity testing, medicine and genetic anal. Thus, total 588 SNPs were identified in 212 genes relevant to **cancer**, inflammation, heart diseases, cardiovascular diseases and microorganisms by sequencing of target sequences from individuals of diverse ethnic and geog. backgrounds by **hybridization** to probes immobilized to microfabricated arrays.

L7 ANSWER 12 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 20 May 2001
ACCESSION NUMBER: 2001:363616 CAPLUS
DOCUMENT NUMBER: 136:113604
TITLE: **Amplification** and expression of splice variants of the gene encoding the P450 cytochrome **25-hydroxyvitamin** D3 1,α-

hydroxylase (CYP 27B1) in human malignant glioma

AUTHOR(S): Maas, Ruth Maria; Reus, Katrin; Diesel, Britta; Steudel, Wolf-Ingo; Feiden, Wolfgang; Fischer, Ulrike; Meese, Eckart

CORPORATE SOURCE: Institut fur Humangenetik, Theoretische Medizin Universitat des Saarlandes, Homburg/Saar, 66421, Germany

SOURCE: Clinical Cancer Research (2001), 7(4), 868-875
CODEN: CCREF4; ISSN: 1078-0432

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recently, we reported the isolation of six novel genes termed glioma-**amplified** sequences (GASs) from the glioblastoma cell line TX3868 using microdissected mediated cDNA capture (U. Fischer et al., Hum. Mol. Genet., 5: 595-600, 1996). The aim of this study was to further characterize the gene GAS89. To **determine** the **amplification** frequency, we performed comparative PCR studies and Southern blot **hybridization** expts. To identify full-length clones of GAS89 we **screened** a HybriZAP library-Reverse transcription-PCR was performed to isolate splice variants and to **determine** expression levels. We identified for the gene GAS89 an **amplification** frequency of 25% in 28 examined glioblastoma multi-forme samples. **Screening** a HybriZAP library, we isolated an incomplete gene sequence showing identity with the gene for **25-hydroxyvitamin** D3 1,α- **hydroxylase**. Different full-length clones were then isolated using PCR primers chosen from the 3' - and 5' -untranslated regions. As **determined** by sequencing, the clones represent various splice variants of the **25-hydroxyvitamin** D3 1,α- **hydroxylase** gene. The clones encode truncated proteins but also one potentially functional enzyme variant. Reverse transcription-PCR studies revealed overexpression of several variants in glioblastoma samples with GAS89 **amplification** in comparison with normal brain RNA and glioblastoma without GAS89 **amplification**. This is the first report of gene **amplification** for **25-hydroxyvitamin** D3 1,α- **hydroxylase** and the appearance of mRNA splice variants in glioblastoma multi-forme. The endogenous expression of the **25-hydroxyvitamin** D3 1,α- **hydroxylase** gene and the appearance of alternative splice variants reveal a new feature of the mol. pathogenesis of glioblastoma and may represent a new target for glioma therapy.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 11 May 2001

ACCESSION NUMBER: 2001:338762 CAPLUS

DOCUMENT NUMBER: 134:362292

TITLE: Methods of **determining** individual hypersensitivity to a pharmaceutical agent from gene expression profile

INVENTOR(S): Farr, Spencer

PATENT ASSIGNEE(S): Phase-1 Molecular Toxicology, USA

SOURCE: PCT Int. Appl., 222 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001032928	A2	20010510	WO 2000-US30474	20001103
WO 2001032928	A3	20020725		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-165398P P 19991105
US 2000-196571P P 20000411

AB The invention discloses methods, gene databases, gene arrays, protein arrays, and devices that may be used to **determine** the hypersensitivity of individuals to a given agent, such as drug or other chemical, in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetd. to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

L7 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Oct 2000
ACCESSION NUMBER: 2000:725793 CAPLUS
DOCUMENT NUMBER: 133:291918
TITLE: **CYP24** gene **amplification** and its use as marker for presence or progression of or predisposition to **cancer**
INVENTOR(S): Albertson, Donna G.; Pinkel, Daniel; Collins, Colin; Gray, Joe W.; Ystra, Bauke
PATENT ASSIGNEE(S): Regents of the University of California, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000060109	A1	20001012	WO 2000-US5972	20000306
W: CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2367291	AA	20001012	CA 2000-2367291	20000306
EP 1255850	A1	20021113	EP 2000-916145	20000306
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY				

PRIORITY APPLN. INFO.: US 1999-285292 A 19990402
WO 2000-US5972 W 20000306

AB This invention pertains to the discovery that an **amplification** of the **CYP24** gene or an increase in **CYP24** activity is a marker for the presence of, progression of, or predisposition to, a **cancer** (e.g., breast **cancer**). Using this information, this invention provides methods of **detecting** a predisposition to **cancer** in an animal. The methods involve (i) providing a biol. sample from an animal (e.g. a human patient); (ii) **detecting** the level of **CYP24** within the biol. sample; and (iii) comparing the level of **CYP24** with a level of **CYP24** in a control sample taken from a normal, **cancer**-free tissue where an increased level of **CYP24** in the biol. sample compared to the level of **CYP24** in the control sample indicates the presence of said **cancer** in said animal.

IT **53112-53-1, 25-Hydroxyvitamin** D3 24-**hydroxylase**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence)
(**CYP24** gene **amplification** and its use as marker for presence or progression of or predisposition to **cancer**)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 17 Dec 1999
ACCESSION NUMBER: 1999:795994 CAPLUS
DOCUMENT NUMBER: 132:31744
TITLE: Gene probes used for genetic profiling in healthcare **screening** and planning
INVENTOR(S): Roberts, Gareth Wyn
PATENT ASSIGNEE(S): Genostic Pharma Ltd., UK
SOURCE: PCT Int. Appl., 745 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9964627 A2 19991216 WO 1999-GB1780 19990604
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

GB 1998-12099	A	19980606
GB 1998-13291	A	19980620
GB 1998-13611	A	19980624
GB 1998-13835	A	19980627
GB 1998-14110	A	19980701
GB 1998-14580	A	19980707
GB 1998-15438	A	19980716
GB 1998-15574	A	19980718
GB 1998-15576	A	19980718
GB 1998-16085	A	19980724
GB 1998-16086	A	19980724
GB 1998-16921	A	19980805
GB 1998-17097	A	19980807
GB 1998-17200	A	19980808
GB 1998-17632	A	19980814
GB 1998-17943	A	19980819

AB There is considerable evidence that significant factor underlying the individual variability in response to disease, therapy and prognosis lies in a person's genetic make-up. There have been numerous examples relating that polymorphisms within a given gene can alter the functionality of the protein encoded by that gene thus leading to a variable physiol. response. In order to bring about the integration of genomics into medical practice and enable design and building of a technol. platform which will enable the everyday practice of mol. medicine a way must be invented for the DNA sequence data to be aligned with the identification of genes central to the induction, development, progression and outcome of disease or physiol. states of interest. According to the invention, the number of genes and their configurations (mutations and polymorphisms) needed to be identified in order to provide critical clin. information concerning individual prognosis is considerably less than the 100,000 thought to comprise the human genome. The identification of the identity of the core group of genes enables the invention of a design for genetic profiling technologies which comprises of the identification of the core group of genes and their sequence variants required to provide a broad base of clin. prognostic information - "genostics". The "Genostic" profiling of patients and persons will radically enhance the ability of clinicians, healthcare professionals and other parties to plan and manage healthcare provision and the targeting of appropriate healthcare resources to those deemed most in need. The use of this invention could also lead to a host of new applications for such profiling technologies, such as identification of persons with particular work or environment related risk, selection of applicants for employment, training or specific opportunities or for the enhancing of the planning and organization of health services, education services and social services.

L7 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 17 Dec 1999
ACCESSION NUMBER: 1999:795993 CAPLUS
DOCUMENT NUMBER: 132:31743
TITLE: Gene probes used for genetic profiling in healthcare **screening** and planning
INVENTOR(S): Roberts, Gareth Wyn
PATENT ASSIGNEE(S): Genostic Pharma Limited, UK
SOURCE: PCT Int. Appl., 149 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9964626	A2	19991216	WO 1999-GB1779	19990604
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2330929	AA	19991216	CA 1999-2330929	19990604
AU 9941586	A1	19991230	AU 1999-41586	19990604
AU 766544	B2	20031016		
AU 9941587	A1	19991230	AU 1999-41587	19990604
GB 2339200	A1	20000119	GB 1999-12914	19990604
GB 2339200	B2	20010912		
EP 1084273	A1	20010321	EP 1999-925207	19990604
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003528564	T2	20030930	JP 2000-553616	19990604
US 2003198970	A1	20031023	US 2002-206568	20020729

PRIORITY APPLN. INFO.:	GB 1998-12098	A 19980606
	GB 1998-28289	A 19981223
	GB 1998-16086	A 19980724
	GB 1998-16921	A 19980805
	GB 1998-17097	A 19980807
	GB 1998-17200	A 19980808
	GB 1998-17632	A 19980814
	GB 1998-17943	A 19980819
	US 1999-325123	B1 19990603
	WO 1999-GB1779	W 19990604

AB There is considerable evidence that significant factor underlying the individual variability in response to disease, therapy and prognosis lies in a person's genetic make-up. There have been numerous examples relating that polymorphisms within a given gene can alter the functionality of the protein encoded by that gene thus leading to a variable physiol. response. In order to bring about the integration of genomics into medical practice and enable design and building of a technol. platform which will enable the everyday practice of mol. medicine a way must be invented for the DNA sequence data to be aligned with the identification of genes central to

the induction, development, progression and outcome of disease or physiol. states of interest. According to the invention, the number of genes and their configurations (mutations and polymorphisms) needed to be identified in order to provide critical clin. information concerning individual prognosis is considerably less than the 100,000 thought to comprise the human genome. The identification of the identity of the core group of genes enables the invention of a design for genetic profiling technologies.

L7 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 03 May 1999
ACCESSION NUMBER: 1999:270435 CAPLUS
DOCUMENT NUMBER: 131:53709
TITLE: Liarozole acts synergistically with 1α,25-dihydroxyvitamin D3 to inhibit growth of DU 145 human prostate **cancer** cells by blocking 24-hydroxylase activity
AUTHOR(S): Ly, Lan H.; Zhao, Xiao-Yan; Holloway, Leah; Feldman, David
CORPORATE SOURCE: Department of Medicine, Division of Endocrinology, Stanford University School of Medicine, Stanford, CA, 94305, USA
SOURCE: Endocrinology (1999), 140(5), 2071-2076
CODEN: ENDOAO; ISSN: 0013-7227
PUBLISHER: Endocrine Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB 1α,25-Dihydroxyvitamin D3 [1,25-(OH)2D3] inhibits the proliferation of many **cancer** cells in culture, but not the aggressive human prostate **cancer** cell line DU 145. We postulated that the 1,25-(OH)2D3-resistant phenotype in DU 145 cells might result from the high levels of expression of **25-hydroxyvitamin** D-24-**hydroxylase** (24-**hydroxylase**) induced by treatment with 1,25-(OH)2D3. As this P 450 enzyme initiates 1,25-(OH)2D3 catabolism, we presumed that a high level of enzyme induction could limit the effectiveness of the 1,25-(OH)2D3 antiproliferative action. To examine this hypothesis we explored combination therapy with liarozole fumarate (R85,246), an imidazole derivative currently in trials for prostate **cancer** therapy. As imidizole derivs. are known to inhibit P 450 enzymes, we postulated that this drug would inhibit 24-hydroxylase [illegible] 25-(OH)2D3 half-life, thereby enhancing [illegible]ive effects on DU 145 cells. Cell growth was [illegible] viable cells using the MTS assay. [illegible]25-(OH)2D3 (1-10 nm) nor liarozole (1-10 μM) [illegible]h. However, when added together, 1,25-(OH)2D3 [illegible]hibited growth 65% after 4 days of culture. [illegible]ess 24-hydroxylase activity and demonstrated [illegible]nhibited this P 450 enzyme in a [illegible]eover, liarozole treatment caused a significant [illegible]lf-life from 11 to 31 h. In addition, [illegible]logous up-regulation of the vitamin D receptor [illegible]of liarozole, this effect was **amplified** [illegible]D3 activity. Western blot analyses [illegible]lls treated with 1,25-(OH)2D3/liarozole showed [illegible]han cells treated with either drug alone. In [illegible]te that liarozole augments the ability of

Shears 571-272-2528

1,25-(OH)2D3 to inhibit DU 145 cell growth. The mechanism appears to be due to inhibition of 24-hydroxylase activity, leading to increased 1,25-(OH)2D3 half-life and augmentation of homologous up-regulation of VDR. We raise the possibility that combination therapy using 1,25-(OH)2D3 and liarozole or other inhibitors of 24-hydroxylase, both in nontoxic doses, might serve as an effective treatment for prostate **cancer**
.

IT **53112-53-1, 25-Hydroxyvitamin** D-24-**hydroxylase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(liarozole synergism with dihydroxyvitamin D3 in prostate **cancer** inhibition: hydroxylase blocking)

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 14:39:37 ON 01 FEB 2005)
L8 32 S L7
L9 14 DUP REM L8 (18 DUPLICATES REMOVED)

L9 ANSWER 1 OF 14 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004058250 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14760115
TITLE: Clinical significance of the overexpression of the candidate oncogene **CYP24** in esophageal **cancer**.
AUTHOR: Mimori K; Tanaka Y; Yoshinaga K; Masuda T; Yamashita K; Okamoto M; Inoue H; Mori M
CORPORATE SOURCE: Department of Surgery, Medical Institute of Bioregulation, Kyushu University, Beppu, Japan.
SOURCE: Annals of oncology : official journal of the European Society for Medical Oncology / ESMO, (2004 Feb) 15 (2) 236-41.
Journal code: 9007735. ISSN: 0923-7534.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200406
ENTRY DATE: Entered STN: 20040205
Last Updated on STN: 20040602
Entered Medline: 20040601

AB BACKGROUND: By using array comparative genomic **hybridization** (**CGH**), the increased copy number of **CYP24** (which encodes vitamin D 24-hydroxylase) at 20q13.2 was previously reported, leading to the identification of **CYP24** as a candidate oncogene in breast **cancer**. **CYP24** leads to abrogate growth control mediated by vitamin D. MATERIALS AND METHODS: We examined **CYP24** expression as well as VDR (vitamin D receptor) gene expression in 42 esophageal **cancer** cases using semi-**quantitative** RT-PCR assay. We induced **CYP24** in seven esophageal **cancer** cell lines using 25-hydroxyvitamin D3 [25(OH)D3] and compared cell growth rate, **measured** using the 3-(4, 5-dimethylthiazol-2-y)-2, 5-diphenyltetrazolium bromide (MTT) assay system. RESULTS: The overall survival rate was significantly higher in 25 cases of lower **CYP24**

expression than 17 cases of higher **CYP24** expression (P <0.05); on the other hand, 23 cases of low VDR expression had a poorer prognosis than 19 cases of high VDR expression. Moreover, we disclosed that the inverse correlation between **CYP24** and VDR expression is significant in esophageal **cancer** cases (P <0.05). Furthermore, the cell growth evaluated by MTT assay was greatly increased in **CYP24**-induced and VDR-diminished cells than non-responding cells by 25(OH)D3 activity (P <0.01). CONCLUSIONS: Overexpression of the candidate oncogene **CYP24** is inversely correlated to vitamin D receptor expression, and may play an important role in **determination** of the malignant potential of esophageal **cancer**.

L9 ANSWER 2 OF 14 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN DUPLICATE 2

ACCESSION NUMBER: 2004:395116 BIOSIS
DOCUMENT NUMBER: PREV200400398579
TITLE: No evidence for **amplification** of 25-hydroxyvitamin D-1alpha-OHase (1alpha-OHase) or 1,25-dihydroxyvitamin D-24-OHase (24-OHase) genes in malignant melanoma (MM).
AUTHOR(S): Reichrath, Jorg [Reprint Author]; Rafi, Leyla; Rech, Martin; Meineke, Viktor; Tilgen, Wolfgang; Seifert, Markus
CORPORATE SOURCE: Dept Dermatol, Saarland Univ Hosp, Kirrberger Str, D-66421, Homburg, Germany
hajrei@uniklinik-saarland.de
SOURCE: Journal of Steroid Biochemistry and Molecular Biology, (May 2004) Vol. 89-9, No. 1-5, pp. 163-166. print.
CODEN: JSBBEZ. ISSN: 0960-0760.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 13 Oct 2004
Last Updated on STN: 13 Oct 2004

AB Increasing evidence points at an important function of Vitamin D metabolites for growth regulation in various tissues, including MM. Using array **CGH**, **amplification** of 24-OHase was recently **detected** as a likely target oncogene of the **amplification** unit 20q13.2 in breast **cancer** cell lines and **tumors**. Additionally, **amplification** of 1alpha-OHase has been reported in human malignant glioma. Using immunohistochemistry, we have now **detected** nuclear Vitamin D receptor (VDR) immunoreactivity in primary cutaneous malignant melanoma (MM), indicating that Vitamin D metabolites may be of importance for the growth regulation in these **tumors**. Using Southern analysis, we have analyzed MM and metastases for evidence of **amplification** of 1alpha-OHase or 24-OHase genes. Our results do not support the hypothesis that **amplification** of 1alpha-OHase or 24-OHase genes may be of importance for pathogenesis or progression of MM.

L9 ANSWER 3 OF 14 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 2003338018 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12845628
TITLE: **Determination** of amplicon boundaries at 20q13.2 in tissue samples of human gastric adenocarcinomas by high-resolution microarray comparative genomic

hybridization.

AUTHOR: Weiss Marjan M; Snijders Antoine M; Kuipers Ernst J; Ylstra Bauke; Pinkel Daniel; Meuwissen Stefan G M; van Diest Paul J; Albertson Donna G; Meijer Gerrit A
CORPORATE SOURCE: Department of Gastroenterology, VU University Medical Centre, Amsterdam, The Netherlands.
CONTRACT NUMBER: CA80314 (NCI)
CA83040 (NCI)
SOURCE: Journal of pathology, (2003 Jul) 200 (3) 320-6.
Journal code: 0204634. ISSN: 0022-3417.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200309
ENTRY DATE: Entered STN: 20030722
Last Updated on STN: 20030917
Entered Medline: 20030916

AB Comparative genomic **hybridization** (**CGH**) of gastric adenocarcinomas frequently shows gains and **amplifications** of chromosome 20. However, the underlying genetic lesion is unknown and conventional **CGH** results do not allow specification of the target region. In order to investigate this chromosomal aberration with a higher resolution and sensitivity, microarray-based **CGH** was performed with both scanning and high-resolution arrays of chromosome 20 in a series of 27 gastric adenocarcinomas. Locus-specific fragments of genomic DNA from bacterial artificial chromosome (BAC) clones were spotted as microarrays. A scanning array contained a set of 27 BAC clones covering chromosome 20q. A high-resolution array contained 27 overlapping BAC clones at 20q13.2. This high-resolution array was used to narrow down the amplicon at 20q13.2 in **tumours** showing **amplification** of this chromosomal region with the scanning array. Positive copy number changes on chromosome 20q were **detected** in 12 of 27 cases (44%). These changes included gain of the whole arm of chromosome 20q in 8 of 27 (30%) cases, **amplification** restricted to 20q12.1 in one case, and **amplifications** restricted to 20q13 in three cases (11%). The three **tumours** showing **amplification** restricted to 20q13 were analysed further using the high-resolution array. In one **tumour**, the whole contig was **amplified** at a constant level. One of the other two **tumours** had a clear proximal breakpoint, while the other **tumour** had a clear distal breakpoint within the 20q13.2 region. The proximal and the distal breakpoint were approximately 800 kb apart. In the present study, an amplicon at 20q13.2 has been narrowed down to 800 kb which is likely to harbour one or more putative oncogenes relevant to gastric **carcinogenesis**, for which ZNF217 and **CYP24** are good candidates.

L9 ANSWER 4 OF 14 MEDLINE on STN
ACCESSION NUMBER: 2003365212 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12899522
TITLE: Combination of vitamin D metabolites with selective inhibitors of vitamin D metabolism.
AUTHOR: Schuster Inge; Egger Helmut; Reddy G Satyanarayana; Vorisek Georg
CORPORATE SOURCE: Institute of Pharmaceutical Chemistry, University Vienna,

Althanstrasse 15, 1090 Vienna, Austria..
inge@tbi.univie.ac.at
SOURCE: Recent results in cancer research. Fortschritte der Krebsforschung. Progres dans les recherches sur le cancer, (2003) 164 169-88. Ref: 43
Journal code: 0044671. ISSN: 0080-0015.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200312
ENTRY DATE: Entered STN: 20030806
Last Updated on STN: 20031218
Entered Medline: 20031204

AB 1alpha,25(OH)2D3 exerts antiproliferative, differentiating effects on many cell types, including **cancer** tissues. In most of its target cells, levels of 1alpha,25(OH)2D3 are regulated by local synthesis via CYP27B and metabolism via **CYP24**. Rapidly induced by vitamin D, **CYP24** repeatedly hydroxylates the vitamin D side chain and ultimately terminates hormonal activity. Aiming at increased hormone levels, lifetime and function, numerous vitamin D analogs have been synthesized with structural modifications, which impede oxidation of the vitamin D side chain. Our group followed a different strategy, namely, blocking 1,25(OH)2D3 metabolism with inhibitors of **CYP24**. As appropriate inhibitors, we exploited compounds termed azoles, which directly bind to the heme iron of the CYPs via an azole nitrogen and to other parts of the substrate site. We synthesized some 400 azoles and tested their potential to selectively inhibit **CYP24**, but not hormone synthesis by the related CYP27B. Using primary human keratinocyte cultures as the source of **CYP24** and CYP27, we discovered some 50 inhibitors of **CYP24** with IC50 values in the nanomole range and selectivities up to 60-fold. As the first representative of selective **CYP24** inhibitors, VID400 underwent preclinical development. In human keratinocytes, VID400 stabilized levels of endogenously produced 1alpha,25(OH)2D3, and thereby strongly **amplified** and prolonged expression of **CYP24**, a surrogate marker of hormonal function. In parallel, antiproliferative activity showed up at 100-fold or more lower concentrations of 1alpha,25(OH)2D3. This data suggests that **CYP24** inhibitors could become attractive drugs in antiproliferative therapy, used as single entities to increase or extend endogenous hormone function or in combination with low doses of potent analogs. Moreover, we used selective inhibitors as valuable tools to (a) elucidate regulatory mechanisms of vitamin D synthesis and metabolism, (b) **determine** intrinsic activities of the otherwise highly transient vitamin D metabolites and (c) model the active sites of **CYP24** and CYP27B.

L9 ANSWER 5 OF 14 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-643397 [69] WPIDS
DOC. NO. CPI: C2004-014240
TITLE: New genetic variants of the human polypeptide 1 (CYP27B1) gene, useful for treating disorders associated with aberrant expression or overproduction of TNF e.g. **cancer**, diabetes or inflammatory disorders.

DERWENT CLASS: B04 D16
INVENTOR(S): BIEGLECKI, K M; KAZEMI, A; MONROE, G; SHAH, N
PATENT ASSIGNEE(S): (GENA-N) GENAISSANCE PHARM INC
COUNTRY COUNT: 97
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002062820	A2	20020815	(200269)*	EN	64
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2002251686	A1	20020819	(200427)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002062820	A2	WO 2001-US47438	20011105
AU 2002251686	A1	AU 2002-251686	20011105

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002251686	A1	Based on	WO 2002062820

PRIORITY APPLN. INFO: US 2000-245797P 20001103
AN 2002-643397 [69] WPIDS
AB WO 200262820 A UPAB: 20040505
NOVELTY - Isolated polynucleotide (I) comprising a coding sequence for a CYP27B1 isogene with the regions of a fully defined sequence of 1527 bp, defined by exons 1 and 3-9, except at each of the polymorphic sites (PS), referred to as PS3-4 to designate the order in which they are located in the gene, is new.

DETAILED DESCRIPTION - The isolated polynucleotide comprises a nucleotide sequence consisting of:

(a) a first nucleotide sequence comprising a cytochrome P450, subfamily XXVIIB (**25-hydroxyvitamin** D-1-alpha-**hydroxylase**) or CYP27B1 isogene; and

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence. The CYP27B1 isogene is selected from fully defined isogenes 1-2 and 4-8. Each of the isogenes comprises the regions of a fully defined sequence of 5547 bp (I) and is further defined by the corresponding sequence of polymorphisms whose positions and locations are fully described in the specification.

INDEPENDENT CLAIMS are also included for:

(1) haplotyping (M1) P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene of an individual;

(2) genotyping (M2) P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene of an individual;

(3) predicting (M3) a haplotype pair for the CYP27B1 gene of an individual;

(4) identifying (M4) an association between a trait and at least one haplotype or haplotype pair of the P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene;

(5) an isolated nucleotide designed for **detecting** a polymorphism in the P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene at a PS selected from PS-7; where the selected PS have the position and alternative alleles shown in (I);

(6) a kit for haplotyping or genotyping P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene of an individual;

(7) a recombinant nonhuman organism, which is transformed or transfected with the isolated polynucleotide and which expresses a P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 protein that is encoded by the first nucleotide or polymorphic variant sequence;

(8) an isolated fragment of a P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 isogene, which comprises at least 10 nucleotides in one of the regions of (I) and one or more polymorphisms consisting of thymine at PS1 or PS6, guanine at PS2 or PS4, adenine at PS3 or cytosine at PS5 or PS7;

(9) an isolated fragment of a CYP27B1 coding sequence, which comprises one or more polymorphisms consisting of adenine at position 942 and guanine at position 1057 of (II);

(10) an isolated polypeptide, which comprises a sequence that is a polymorphic variant of a reference sequence having 508 amino acids, for the P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 protein, encoded by exons 1 and 3-9, except the polymorphic variant comprising alanine at position 353;

(11) an isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide;

(12) **screening** (M5) for drugs or other chemical compounds that bind to or are enzymatic substrates for the isolated polypeptide;

(13) an isolated fragment of a CYP27B1 protein, comprising alanine at position 353 of the reference sequence;

(14) a computer system for storing and analyzing polymorphism data for the P450, **25-hydroxyvitamin** D-1-alpha-**hydroxylase** or CYP27B1 gene; and

(15) a genome anthology for the CYP27B1 gene, comprising 2 or more of the CYP27B1 isogenes 1-8 in the Index Repository fully described in the specification.

ACTIVITY - Cytostatic; Antidiabetic; Antiinflammatory.

No suitable data given.

MECHANISM OF ACTION - Gene therapy.

USE - The pharmaceutical composition, comprising the isolated polynucleotide, an antisense oligonucleotide directed against one of the novel CYP27B1 isogenes, a polynucleotide encoding the antisense oligonucleotide or another compound that inhibits expression of the CYP27B1 isogene, is useful for treating disorders affected by expression or function of the TNF isogene e.g. **cancer**, diabetes or inflammatory disorders.

Dwg.0/3

L9 ANSWER 6 OF 14 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2002153187 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11856765
TITLE: Synthesis of 1,25-dihydroxyvitamin D(3) by human

endothelial cells is regulated by inflammatory cytokines: a novel autocrine **determinant** of vascular cell adhesion.

AUTHOR: Zehnder Daniel; Bland Rosemary; Chana Ravinder S; Wheeler David C; Howie Alexander J; Williams Mary C; Stewart Paul M; Hewison Martin

CORPORATE SOURCE: Division of Medical Sciences, The University of Birmingham, Queen Elizabeth Hospital, Birmingham, UK.

SOURCE: Journal of the American Society of Nephrology : JASN, (2002 Mar) 13 (3) 621-9.
Journal code: 9013836. ISSN: 1046-6673.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200204

ENTRY DATE: Entered STN: 20020312
Last Updated on STN: 20020429
Entered Medline: 20020426

AB In addition to its calciotropic function, the secosteroid 1,25-dihydroxyvitamin D(3) (1,25(OH)(2)D(3)) has potent nonclassical effects. In particular, local production of 1,25D(3) catalyzed by the enzyme 1alpha-hydroxylase (1alpha-OHase) may act as an autocrine/paracrine immunomodulatory mechanism. To investigate the significance of this in vascular tissue the expression and function of 1alpha-OHase in human endothelial cells was characterized. Immunohistochemical and in situ **hybridization** analyses show, for the first time, the presence of 1alpha-OHase mRNA and protein in endothelial cells from human renal arteries as well as postcapillary venules from lymphoid tissue. Reverse transcription-PCR and Western blot analyses confirmed the presence of 1alpha-OHase in primary cultures of human umbilical vein endothelial cells (HUVEC). Enzyme activity in HUVEC (318 +/- 56 fmoles 1,25(OH)(2)D(3)/hr/mg protein) increased after treatment with **tumor** necrosis factor-alpha (1054 +/- 166, $P < 0.01$), lipopolysaccharide (1381 +/- 88, $P < 0.01$), or forskolin (554 +/- 56, $P < 0.05$). Functional studies showed that exogenously added 1,25(OH)(2)D(3) or its precursor, 25-hydroxyvitamin D(3) (25(OH)D(3)), significantly decreased HUVEC proliferation after 72 h of treatment (33% and 11%, respectively). In addition, after 24 h treatment, both 1,25(OH)(2)D(3) and 25(OH)D(3) increased the adhesion of monocytic U937 cells to HUVEC (159% and 153%, respectively). These data indicate that human endothelia are able to produce active vitamin D. The rapid induction of endothelial 1alpha-OHase activity by inflammatory cytokines suggests a novel autocrine/paracrine role for the enzyme, possibly as a modulator of endothelial cell adhesion.

L9 ANSWER 7 OF 14 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 2001219509 MEDLINE

DOCUMENT NUMBER: PubMed ID: 11309335

TITLE: **Amplification** and expression of splice variants of the gene encoding the P450 cytochrome **25-hydroxyvitamin** D(3) 1,alpha-**hydroxylase** (CYP 27B1) in human malignant glioma.

AUTHOR: Maas R M; Reus K; Diesel B; Steudel W I; Feiden W; Fischer U; Meese E

CORPORATE SOURCE: Institut fur Humangenetik, Theoretische Medizin,

Universitat des Saarlandes, 66421 Homburg/Saar, Germany.
SOURCE: Clinical cancer research : an official journal of the American Association for Cancer Research, (2001 Apr) 7 (4) 868-75.
Journal code: 9502500. ISSN: 1078-0432.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010618
Last Updated on STN: 20010618
Entered Medline: 20010614

AB PURPOSE: Recently, we reported the isolation of six novel genes termed glioma-**amplified** sequences (GASs) from the glioblastoma cell line TX3868 using microdissected mediated cDNA capture (U. Fischer et al., HUM: MOL: GENET:, 5: 595-600, 1996). The aim of this study was to further characterize the gene GAS89. EXPERIMENTAL DESIGN: To **determine** the **amplification** frequency, we performed comparative PCR studies and Southern blot **hybridization** experiments. To identify full-length clones of GAS89 we **screened** a HybriZAP library. Reverse transcription-PCR was performed to isolate splice variants and to **determine** expression levels. RESULTS: We identified for the gene GAS89 an **amplification** frequency of 25% in 28 examined glioblastoma multiforme samples. **Screening** a HybriZAP library, we isolated an incomplete gene sequence showing identity with the gene for **25-hydroxyvitamin** D(3) 1,alpha-**hydroxylase**. Different full-length clones were then isolated using PCR primers chosen from the 3'- and 5'-untranslated regions. As **determined** by sequencing, the clones represent various splice variants of the **25-hydroxyvitamin** D(3) 1,alpha-**hydroxylase** gene. The clones encode truncated proteins but also one potentially functional enzyme variant. Reverse transcription-PCR studies revealed overexpression of several variants in glioblastoma samples with GAS89 **amplification** in comparison with normal brain RNA and glioblastoma without GAS89 **amplification**. CONCLUSIONS: This is the first report of gene **amplification** for **25-hydroxyvitamin** D(3) 1,alpha-**hydroxylase** and the appearance of mRNA splice variants in glioblastoma multiforme. The endogenous expression of the **25-hydroxyvitamin** D(3) 1,alpha-**hydroxylase** gene and the appearance of alternative splice variants reveal a new feature of the molecular pathogenesis of glioblastoma and may represent a new target for glioma therapy.

L9 ANSWER 8 OF 14 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 2001339134 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11242591
TITLE: A **quantitative** trait locus influencing estrogen levels maps to a region homologous to human chromosome 20.
AUTHOR: Martin L J; Blangero J; Rogers J; Mahaney M C; Hixson J E; Carey K D; Morin P A; Comuzzie A G
CORPORATE SOURCE: Departments of Genetics, Physiology and Medicine, Southwest Foundation for Biomedical Research San Antonio, Texas 78245-0549, USA.. lmartin@darwin.sfbr.org
CONTRACT NUMBER: HL-28972 (NHLBI)
SOURCE: Physiological genomics, (2001 Mar 8) 5 (2) 75-80.

Journal code: 9815683. ISSN: 1531-2267.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010618
Last Updated on STN: 20030123
Entered Medline: 20010614

AB Estrogen, a steroid hormone, regulates reproduction and has been implicated in several diseases. We performed a genome-wide scan using multipoint linkage analysis implemented in a general pedigree-based variance component approach to identify genes with **measurable** effects on variation in estrogen levels in baboons. A microsatellite polymorphism, D20S171, located on human chromosome 20q13.11, showed strong evidence of linkage with a LOD score of 3.06 (P = 0.00009). This region contains several potential candidate genes including melanocortin 3 receptor (MC3R), cytochrome P-450 subfamily XXIV (**CYP24**), and breast **carcinoma amplified** sequence (BCAS1). This is the first evidence of a **quantitative** trait locus with a significant effect on estrogen.

L9 ANSWER 9 OF 14 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-656233 [63] WPIDS
DOC. NO. NON-CPI: N2000-486463
DOC. NO. CPI: C2000-198633
TITLE: **Detecting** a predisposition to or a progression of **cancer** especially breast **cancer** in humans comprises **detecting** levels of **CYP24** in a biological sample.
DERWENT CLASS: B04 C07 D16 S03
INVENTOR(S): ALBERTSON, D G; COLLINS, C; GRAY, J W; PINKEL, D; YSTRA, B
PATENT ASSIGNEE(S): (REGC) UNIV CALIFORNIA
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000060109	A1	20001012	(200063)*	EN	73
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP					
EP 1255850	A1	20021113	(200282)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
JP 2002540798	W	20021203	(200309)		93

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000060109	A1	WO 2000-US5972	20000306
EP 1255850	A1	EP 2000-916145	20000306
		WO 2000-US5972	20000306
JP 2002540798	W	JP 2000-609598	20000306
		WO 2000-US5972	20000306

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1255850	A1 Based on	WO 2000060109
JP 2002540798	W Based on	WO 2000060109

PRIORITY APPLN. INFO: US 1999-285292 19990402
AN 2000-656233 [63] WPIDS
AB WO 200060109 A UPAB: 20001205
NOVELTY - **Detecting** (I) a predisposition to **cancer** in an animal, comprises **detecting** the level of **CYP24** (**25-hydroxyvitamin** D3 24-**hydroxylase** enzyme) in a biological sample from the animal and comparing it with a control sample taken from a normal, **cancer**-free tissue, where an increased level of **CYP24** in the biological sample compared to the control sample indicates a predisposition to **cancer** in the animal.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) treating (II) **cancer** in an animal, comprising (I) and selecting and performing a **cancer** therapy in those animals having an increased level of **CYP24** compared to the level of **CYP24** in the control sample;

(2) **screening** (III) a test agent for its ability to inhibit proliferation of a **CYP24**-expressing cell, comprising contacting the **CYP24** expressing cell with the test agent and **detecting** the level of **CYP24** activity, where a decreased level of **CYP24** activity as compared to the level of **CYP24** activity in a cell not contacted with the agent indicates that the agent inhibits proliferation of the cell;

(3) decreasing (IV) the proliferation of a cell with an elevated level of **CYP24**, by reducing the level of **CYP24** activity in the cell using an inhibitor of **CYP24**; and

(4) estimating the survival expectancy of an animal with **cancer** by performing (I), where an increased level of **CYP24** in the biological sample compared to the control sample indicates a reduced survival expectancy in the animal.

ACTIVITY - Cytostatic. No biological data is given.

MECHANISM OF ACTION - **CYP24** modulator.

USE - (I) is useful for **detecting** a predisposition to **cancer** in humans, non-human primates, canines, felines, murines, bovines, equines, porcines and lagomorphs (claimed).

Dwg.0/3

L9 ANSWER 10 OF 14 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2000:275749 BIOSIS
DOCUMENT NUMBER: PREV200000275749
TITLE: Identification of vitamin D 24 hydroxylase (**CYP24**) as a candidate oncogene by microarray **CGH** and **quantitative** expression analysis.
AUTHOR(S): Ylstra, Bauke [Reprint author]; Livezey, Kristin W. [Reprint author]; Albertson, Donna G. [Reprint author]
CORPORATE SOURCE: UCSF Cancer Ctr, San Francisco, CA, USA
SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2000) No. 41, pp. 859. print.

Searcher : Shears 571-272-2528

Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 01-05, 2000.
ISSN: 0197-016X.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 30 Jun 2000
Last Updated on STN: 7 Jan 2002

L9 ANSWER 11 OF 14 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 2000296614 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10835626
TITLE: **Quantitative** mapping of amplicon structure by array **CGH** identifies **CYP24** as a candidate oncogene.
AUTHOR: Albertson D G; Ylstra B; Segraves R; Collins C; Dairkee S H; Kowbel D; Kuo W L; Gray J W; Pinkel D
CORPORATE SOURCE: [1] Cancer Research Institute, University of California, San Francisco, Box 0808, San Francisco, California, USA.. albertson@cc.ucsf.edu
CONTRACT NUMBER: CA45919 (NCI)
CA80314 (NCI)
HD17665 (NICHD)
+
SOURCE: Nature genetics, (2000 Jun) 25 (2) 144-6.
Journal code: 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000706
Last Updated on STN: 20000706
Entered Medline: 20000629

AB We show here that **quantitative measurement** of DNA copy number across **amplified** regions using array comparative genomic **hybridization** (**CGH**) may facilitate oncogene identification by providing precise information on the locations of both amplicon boundaries and **amplification** maxima. Using this analytical capability, we resolved two regions of **amplification** within an approximately 2-Mb region of recurrent aberration at 20q13.2 in breast **cancer**. The putative oncogene ZNF217 (reference 5) mapped to one peak, and **CYP24** (encoding vitamin D 24 hydroxylase), whose overexpression is likely to lead to abrogation of growth control mediated by vitamin D, mapped to the other.

L9 ANSWER 12 OF 14 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-053262 [04] WPIDS
CROSS REFERENCE: 2001-343487 [36]
DOC. NO. CPI: C2000-013911
TITLE: New polypeptides involved in the regulation of phosphate metabolism useful for diagnosing and treating disorders related to phosphate metabolism.
DERWENT CLASS: B04 D16
INVENTOR(S): ROWE, P; ROWE, P S N; ROWE, P S

PATENT ASSIGNEE(S): (UNLO) UNIV COLLEGE LONDON; (ROWE-I) ROWE P S N
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9960017	A2	19991125	(200004)*	EN	136
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
GB 2339572	A	20000202	(200008)		
AU 9943624	A	19991206	(200019)		
EP 1086225	A2	20010328	(200118)	EN	
R: AT BE CH DE DK ES FI FR GB IE IT LI NL SE					
CN 1308677	A	20010815	(200174)		
JP 2002515232	W	20020528	(200238)		149
AU 765349	B	20030918	(200370)		
MX 2000011272	A1	20030401	(200415)		
US 2004053389	A1	20040318	(200421)		
US 6818745	B1	20041116	(200476)		
US 2005014187	A1	20050120	(200507)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9960017	A2		WO 1999-EP3403	19990518
GB 2339572	A		GB 1999-11577	19990518
AU 9943624	A		AU 1999-43624	19990518
EP 1086225	A2		EP 1999-926320	19990518
			WO 1999-EP3403	19990518
CN 1308677	A		CN 1999-806361	19990518
JP 2002515232	W		WO 1999-EP3403	19990518
			JP 2000-549635	19990518
AU 765349	B		AU 1999-43624	19990518
MX 2000011272	A1		WO 1999-EP3403	19990518
			MX 2000-11272	20001116
US 2004053389	A1	Cont of	US 1999-434185	19991104
		CIP of	US 2002-132920	20020425
			US 2003-438181	20030513
US 6818745	B1		WO 1999-EP3403	19990518
			US 2001-700696	20010612
US 2005014187	A1	Div ex	WO 1999-EP3403	19990518
		Div ex	US 2001-700696	20010612
			US 2004-920788	20040817

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9943624	A	Based on	WO 9960017
EP 1086225	A2	Based on	WO 9960017
JP 2002515232	W	Based on	WO 9960017

Searcher : Shears 571-272-2528

AU 765349	B	Previous Publ.	AU 9943624
		Based on	WO 9960017
MX 2000011272	A1	Based on	WO 9960017
US 6818745	B1	Based on	WO 9960017
US 2005014187	A1	Div ex	US 6818745

PRIORITY APPLN. INFO: GB 1998-19387 19980904; GB 1998-10681 19980518

AN 2000-053262 [04] WPIDS

CR 2001-343487 [36]

AB WO 9960017 A UPAB: 20050128

NOVELTY - An isolated polypeptide (P1) having phosphatonin activity.

DETAILED DESCRIPTION - The polypeptide (P1) or an immunologically and/or biologically fragment comprises an amino acid sequence encoded by polynucleotides:

(a) encoding at least the mature form of the polypeptide comprising the amino acid sequence (I), fully defined in the specification;

(b) comprising the coding sequence (II);

(c) encoding a polypeptide having substitution, deletion and/or addition of one or several amino acids of the amino acid sequence encoded by (a) or (b);

(d) comprising the complementary strand which **hybridizes** with a polynucleotide (a), (b) or (c);

(e) encoding a polypeptide with 60% identity to (a)-(d);

(f) encoding a polypeptide capable of regulating phosphate metabolism comprising a fragment or an epitope-bearing portion of a polypeptide encoded by a polynucleotide of any of (a) to (e);

(g) encoding an epitope-bearing portion of a phosphatonin polypeptide comprising amino acid residues from about 1-40, 141-180 and/or 401-429 in sequence (I);

(h) comprising at least 15 nucleotides of a polynucleotide of any of (a) to (g) and encoding a polypeptide capable of regulating phosphate metabolism;

(i) encoding a polypeptide capable of regulating phosphate metabolism comprising the cell and/or glycosaminoglycan attachment motif and/or bone mineral motif of a polypeptide encoded by a nucleotide of any of (a) to (h); and

(j) with a nucleotide sequence which has conservative substitutions to a nucleotide sequence of any of (a) to (i).

INDEPENDENT CLAIMS are also included for the following:

(1) a polynucleotide encoding the polypeptide (P1);

(2) a polynucleotide **hybridizing** with the polynucleotide of (1) and which encodes a mutated version of the polypeptide (P1), lacking at least part of its phosphatonin activity;

(3) a vector containing the polynucleotide of (1) or (2);

(4) a host cell genetically engineered with the polynucleotides of (1) or (2), the vector of (3) or produced by introducing an expression control sequence into a host cell mediating the expression of a gene encoding the polypeptide (P1);

(5) a process for isolating a phosphatonin polypeptide by the following steps:

(a) culturing **tumor**-conditioned media or osteosarcoma cells to confluence in serum supplemented media (DMEM Eagles/10% FCS/glutamine/antimycotic (DMFCS);

(b) incubating the cells on alternate days in serum free media DMEM Eagles/glutamine/antimycotic antibiotic (DM) up to five hours;

(c) collecting conditioned serum free media from the cells and equilibrating the conditioned media to 0.06M sodium phosphate pH 7.2 and 0.5 M NaCl (PBS);

(d) subjecting the media from (c) to an equilibrated column of concanavilin A sepharose;

(e) washing the column extensively with PBS;

(f) eluting the concanavalin A column with PBS supplemented with 0.5M alpha -methyl-D-glucopyranoside;

(g) subjecting the eluted material from (f) to cation exchange chromatography; and

(h) eluting phosphatonin polypeptide containing fractions with 0.5 M NaCl;

(6) a process for producing a polypeptide having the biological and/or immunological activity of phosphatonin by culturing the host cell of (4) and recovering the polypeptide;

(7) polypeptide (P2) obtained by the process of (5) or by proteolytic cleavage of a phosphatonin polypeptide (P1) or by a PHEX metallopeptidase;

(8) an isolated antibody that binds specifically to the polypeptide (P1)/(P2);

(9) a nucleic acid molecule of at least 15 nucleotides which hybridizes specifically with a polynucleotide of (1) or (2) or with a complementary strand;

(10) an isolated regulatory sequence of a promoter regulating the expression of a nucleic acid molecule comprising a polynucleotide of (1) or (2);

(11) a recombinant DNA molecule comprising the regulatory sequence of claim (10);

(12) a method (M2) for identifying a binding partner to a phosphatonin polypeptide by contacting a polypeptide (P1) or (P2) with a compound to be screened, and determining whether the compound effects an activity of the polypeptide;

(13) a method (M3) of identifying and obtaining a drug candidate for therapy of disorders in phosphate metabolism by contacting the polypeptide (P1)/(P2) or a cell expressing the polypeptide in the presence of components capable of providing a detectable signal in response to phosphate uptake, with the drug candidate under conditions which permit phosphate metabolism, and detecting the presence or absence of a signal or increase of the signal generated from phosphate metabolism which is due to the drug;

(14) a method of producing a therapeutic agent which comprises the steps of (13) or (14), and synthesizing the compound identified in step (b) or an analog or derivative in an effective therapeutic amount and combining the compound with a pharmaceutically acceptable carrier; and

(15) an activator/agonist or inhibitor/antagonist of phosphate metabolism or binding partner of phosphatonin by the methods (M1,M2 or M3).

ACTIVITY - Osteopathic;

MECHANISM OF ACTION - Phosphate metabolite.

USE - Polypeptide (P1) or (P2), or the polynucleotides (1) or (2) or the vector of (3) or the antibody of (8), are used to treat phosphate metabolism related disease. Diagnosing a pathological condition or a susceptibility to it, related to a disorder of phosphate metabolism by determining the presence or amount of expression of the polypeptide (P1) or (P2) in a sample. The polypeptide (P1)/(P2) or a DNA encoding and capable of expressing the polypeptide or activator/agonist, binding partner or the antibody, is used in a medicament for treatment of

hyperphosphatemia, or renal osteodystrophy, hyperphophatemia in renal dialysis/pre-dialysis, secondary hyperparathyrodism or osteitis fibrosa cystica, or X-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypercalcuria (HHRH), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophophatemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporosis, vitamin D resistant rickets, end organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide (P1)/(P2) and PHEX metallopeptidase may also be used to manufacture combined preparations for simultaneous, separate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of phosphatonin overexpression is useful for the production of phosphatonin.

DESCRIPTION OF DRAWING(S) - The figure shows p1BL21 and p6XL1 recombinant plasmids containing phosphatonin fusion construct LacI: (lac promoter); LIC: (ligation independent cloning sequence); EK: Enterokinase cleavage site; Thrombin: (thrombin target sequence); Amp: Ampicillin resistance: Cal peptide (calmodulin peptide sequence); Phosphatonin. Dwg.14/14

L9 ANSWER 13 OF 14 MEDLINE on STN DUPLICATE 8

ACCESSION NUMBER: 1999233340 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10218956
TITLE: Liarozole acts synergistically with 1alpha,25-dihydroxyvitamin D3 to inhibit growth of DU 145 human prostate **cancer** cells by blocking 24-hydroxylase activity.
AUTHOR: Ly L H; Zhao X Y; Holloway L; Feldman D
CORPORATE SOURCE: Department of Medicine, Stanford University School of Medicine, California 94305-5103, USA.
CONTRACT NUMBER: DK-42482 (NIDDK)
SOURCE: Endocrinology, (1999 May) 140 (5) 2071-6.
Journal code: 0375040. ISSN: 0013-7227.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 19990517
Entered Medline: 19990506

AB 1Alpha,25-dihydroxyvitamin D3 [1,25-(OH)2D3] inhibits the proliferation of many **cancer** cells in culture, but not the aggressive human prostate **cancer** cell line DU 145. We postulated that the 1,25-(OH)2D3-resistant phenotype in DU 145 cells might result from the high levels of expression of **25-hydroxyvitamin** D-24-**hydroxylase** (24-**hydroxylase**) induced by treatment with 1,25-(OH)2D3. As this P450 enzyme initiates 1,25-(OH)2D3 catabolism, we presumed that a high level of enzyme induction could limit the effectiveness of the 1,25-(OH)2D3 antiproliferative action. To examine this hypothesis we explored combination therapy with liarozole fumarate (R85,246), an imidazole derivative currently in trials for prostate **cancer** therapy. As imidizole derivatives are known to inhibit P450 enzymes, we postulated that this drug would inhibit 24-hydroxylase activity, increasing the 1,25-(OH)2D3 half-life, thereby enhancing 1,25-(OH)2D3 antiproliferative effects on DU 145 cells. Cell growth was

assessed by **measurement** of viable cells using the MTS assay. When used alone, neither 1,25-(OH)2D3 (1-10 nM) nor liarozole (1-10 microM) inhibited DU 145 cell growth. However, when added together, 1,25-(OH)2D3 (10 nM)/liarozole (1 microM) inhibited growth 65% after 4 days of culture. We used a TLC method to assess 24-hydroxylase activity and demonstrated that liarozole (1-100 microM) inhibited this P450 enzyme in a dose-dependent manner. Moreover, liarozole treatment caused a significant increase in 1,25-(OH)2D3 half-life from 11 to 31 h. In addition, 1,25-(OH)2D3 can cause homologous up-regulation of the vitamin D receptor (VDR), and in the presence of liarozole, this effect was **amplified**, thus enhancing 1,25-(OH)2D3 activity. Western blot analyses demonstrated that DU 145 cells treated with 1,25-(OH)2D3/liarozole showed greater VDR up-regulation than cells treated with either drug alone. In summary, our data demonstrate that liarozole augments the ability of 1,25-(OH)2D3 to inhibit DU 145 cell growth. The mechanism appears to be due to inhibition of 24-hydroxylase activity, leading to increased 1,25-(OH)2D3 half-life and augmentation of homologous up-regulation of VDR. We raise the possibility that combination therapy using 1,25-(OH)2D3 and liarozole or other inhibitors of 24-hydroxylase, both in nontoxic doses, might serve as an effective treatment for prostate **cancer**.

L9 ANSWER 14 OF 14 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 1998254107 EMBASE

TITLE: Positional cloning of ZNF217 and NABC1: Genes **amplified** at 20q13.2 and overexpressed in breast **carcinoma**.

AUTHOR: Collins C.; Rommens J.M.; Kowbel D.; Godfrey T.; Tanner M.; Hwang S.- I.; Polikoff D.; Nonet G.; Cochran J.; Myambo K.; Jay K.E.; Froula J.; Cloutier T.; Kuo W.-L.; Yaswen P.; Dairkee S.; Giovanola J.; Hutchinson G.B.; Isola J.; Kallioniemi O.-P.; Palazzolo M.; Martin C.; Ericsson C.; Pinkel D.; Albertson D.; Li W.-B.; Gray J.W.

CORPORATE SOURCE: J.W. Gray, University of California, San Francisco Cancer Center, 2340 Sutter Street, San Francisco, CA 94143-0808, United States. gray@cc.ucsf.edu

SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (21 Jul 1998) 95/15 (8703-8708). Refs: 45
ISSN: 0027-8424 CODEN: PNASA6

COUNTRY: United States

DOCUMENT TYPE: Journal; Conference Article

FILE SEGMENT: 022 Human Genetics

LANGUAGE: English

SUMMARY LANGUAGE: English

AB We report here the molecular cloning of an .simeq.1-Mb region of recurrent **amplification** at 20q13.2 in breast **cancer** and other **tumors** and the delineation of a 260-kb common region of **amplification**. Analysis of the 1-Mb region produced evidence for five genes, ZNF217, ZNF218, and NABC1, PIC1L (PIC1-like), **CYP24**, and a pseudogene CRP (Cyclophillin Related Pseudogene). ZNF217 and NABC1 emerged as strong candidate oncogenes and were characterized in detail. NABC1 is predicted to encode a 585-aa protein of unknown function and is overexpressed in most but not all breast **cancer** cell lines in which it was **amplified**. ZNF217 is centrally located in the

260-kb common region of **amplification**, transcribed in multiple normal tissues, and overexpressed in all cell lines and **tumors** in which it is **amplified** and in two in which it is not. ZNF217 is predicted to encode alternately spliced, Kruppel-like transcription factors of 1,062 and 1,108 aa, each having a DNA-binding domain (eight C2H2 zinc fingers) and a proline-rich transcription activation domain.

(FILE 'CAPLUS' ENTERED AT 14:42:24 ON 01 FEB 2005)

L1 2 SEA FILE=REGISTRY ABB=ON PLU=ON "25-HYDROXYVITAMIN D3 24-HYDROXYLASE"?/CN
L12 266 SEA FILE=CAPLUS ABB=ON PLU=ON 25(W)(HYDROXYVITAMIN OR HYDROXY VITAMIN)(W)D3(W)24(W)HYDROXYLASE
L13 575 SEA FILE=CAPLUS ABB=ON PLU=ON L1 OR L12 OR CYP24 OR CYP 24 OR GENBANK(5A)(U60669 OR U 60669 OR S78775 OR "S 78775")
L14 87 SEA FILE=CAPLUS ABB=ON PLU=ON L13 AND (CANCER? OR CARCIN? OR TUMOUR OR TUMOR OR NEOPLAS?)
L15 38 SEA FILE=CAPLUS ABB=ON PLU=ON L14 AND (DETERM? OR DETECT? OR DET## OR SCREEN? OR MEAS? OR QUANT?)
L16 13 SEA FILE=CAPLUS ABB=ON PLU=ON L15 AND (HYBRIDIS? OR HYBRIDIZ? OR AMPLIF? OR CGH)

L17 0 L16 NOT L7

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 14:50:42 ON 01 FEB 2005)

L18 19 S L16
L19 0 S L18 NOT L8

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 14:53:03 ON 01 FEB 2005)

L20 858 SEA ABB=ON PLU=ON "ALBERTSON D"?/AU
L21 1612 SEA ABB=ON PLU=ON "PINKEL D"?/AU
L22 6432 SEA ABB=ON PLU=ON "COLLINS C"?/AU
L23 14875 SEA ABB=ON PLU=ON "GRAY J"?/AU
L24 2 SEA ABB=ON PLU=ON "YSTRA B"?/AU
L25 2 SEA ABB=ON PLU=ON L20 AND L21 AND L22 AND L23 AND L24
L26 335 SEA ABB=ON PLU=ON L20 AND (L21 OR L22 OR L23 OR L24)
L27 591 SEA ABB=ON PLU=ON L21 AND (L22 OR L23 OR L24)
L28 235 SEA ABB=ON PLU=ON L22 AND (L23 OR L24)
L29 2 SEA ABB=ON PLU=ON L23 AND L24
L30 28 SEA ABB=ON PLU=ON (L26 OR L27 OR L28 OR L20 OR L21 OR L22 OR L23) AND L14
L31 28 SEA ABB=ON PLU=ON L25 OR L29 OR L30
L32 11 DUP REM L31 (17 DUPLICATES REMOVED)

- Author (s)

L32 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2003:799401 CAPLUS
DOCUMENT NUMBER: 140:39712
TITLE: Determination of amplicon boundaries at 20q13.2 in tissue samples of human gastric adenocarcinomas by high-resolution microarray comparative genomic hybridization
AUTHOR(S): Weiss, Marjan M.; Snijders, Antoine M.; Kuipers, Ernst J.; Ylstra, Bauke; **Pinkel, Daniel**; Meuwissen, Stefan G. M.; van Diest, Paul J.; **Albertson, Donna G.**; Meijer, Gerrit A.

CORPORATE SOURCE: Department of Gastroenterology, VU University Medical Centre, Amsterdam, Neth.
SOURCE: Journal of Pathology (2003), 200(3), 320-326
CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Comparative genomic hybridization (CGH) of gastric adenocarcinomas frequently shows gains and amplifications of chromosome 20. However, the underlying genetic lesion is unknown and conventional CGH results do not allow specification of the target region. In order to investigate this chromosomal aberration with a higher resolution and sensitivity, microarray-based CGH was performed with both scanning and high-resolution arrays of chromosome 20 in a series of 27 gastric adenocarcinomas. Locus-specific fragments of genomic DNA from bacterial artificial chromosome (BAC) clones were spotted as microarrays. A scanning array contained a set of 27 BAC clones covering chromosome 20q. A high-resolution array contained 27 overlapping BAC clones at 20q13.2. This high-resolution array was used to narrow down the amplicon at 20q13.2 in **tumors** showing amplification of this chromosomal region with the scanning array. Pos. copy number changes on chromosome 20q were detected in 12 of 27 cases (44%). These changes included gain of the whole arm of chromosome 20q in 8 of 27 (30%) cases, amplification restricted to 20q12.1 in one case, and amplifications restricted to 20q13 in three cases (11%). The three **tumors** showing amplification restricted to 20q13 were analyzed further using the high-resolution array. In one **tumor**, the whole contig was amplified at a constant level. One of the other two **tumors** had a clear proximal breakpoint, while the other **tumor** had a clear distal breakpoint within the 20q13.2 region. The proximal and the distal breakpoint were approx. 800 kb apart. In the present study, an amplicon at 20q13.2 has been narrowed down to 800 kb which is likely to harbor one or more putative oncogenes relevant to gastric **carcinogenesis**, for which ZNF217 and **CYP24** are good candidates.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:754553 CAPLUS
DOCUMENT NUMBER: 137:227626
TITLE: Methods for diagnosing and monitoring malignancies by screening gene copy numbers
INVENTOR(S): Kuo, Wen-Lin; Polikoff, Daniel; **Pinkel, Daniel**; **Albertson, Donna**; Berchuk, Andy; **Gray, Joe W.**
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077197	A2	20021003	WO 2002-US9419	20020327

WO 2002077197 A3 20031023
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2003077582 A1 20030424 US 2001-819148 20010327
PRIORITY APPLN. INFO.: US 2001-819148 A 20010327

AB The invention concerns the discovery that an amplification of some genes or an increase in that gene activity and a deletion of some genes or a decrease in that gene activity is a marker for the presence of, progression of, or predisposition to, a **cancer** (e.g., breast **cancer**). Using this information, this invention provides methods of detecting a predisposition to **cancer** in an animal. The methods involve (i) providing a biol. sample from an animal (e.g. a human patient); (ii) detecting the level of the genes of the present invention within the biol. sample; and (iii) comparing the level of one or more of said genes with a level of one or more of said genes in a control sample taken from a normal, **cancer**-free tissue.

L32 ANSWER 3 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2002:367623 BIOSIS
DOCUMENT NUMBER: PREV200200367623
TITLE: Genome wide array CGH analysis and expression analysis of 47 ductal invasive breast **cancer tumors**.
AUTHOR(S): Ylstra, Bauke [Reprint author]; Olshen, Adam; Snijders, Antoine M.; Segraves, Richard; Zhenhang, Meng; Ginzinger, David; Jain, Ajay N.; **Pinkel, Daniel; Gray, Joe W.**; Dairkee, Shanaz H.; **Albertson, Donna G.**
CORPORATE SOURCE: Free University Medical Center, VUMC, Amsterdam, Netherlands
SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2002) Vol. 43, pp. 288-289. print. Meeting Info.: 93rd Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 06-10, 2002. ISSN: 0197-016X.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Jul 2002
Last Updated on STN: 3 Jul 2002

L32 ANSWER 4 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2002:366339 BIOSIS
DOCUMENT NUMBER: PREV200200366339
TITLE: Genomic evolution in breast **cancer**.

AUTHOR(S): Chen, Koei [Reprint author]; Kuo, Wen-Lin [Reprint author]; Chen, Chira [Reprint author]; **Collins, Colin** [Reprint author]; Volik, Stas [Reprint author]; Jain, Ajay [Reprint author]; **Pinkel, Daniel** [Reprint author]; **Albertson, Donna** [Reprint author]; Waldman, Fredric [Reprint author]; **Gray, Joe W.** [Reprint author]

CORPORATE SOURCE: Comprehensive Cancer Center, University of California, San Francisco, CA, USA

SOURCE: Acta Cytologica, (January-February, 2002) Vol. 46, No. 1 Supplement, pp. 128. print.
Meeting Info.: 14th International Congress of Cytology. Amsterdam, Netherlands. May 27-31, 2001.
CODEN: ACYTAN. ISSN: 0001-5547.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 3 Jul 2002
Last Updated on STN: 3 Jul 2002

L32 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:895110 CAPLUS

DOCUMENT NUMBER: 138:366457

TITLE: Genome scanning with array CGH delineates regional alterations in mouse islet. [Erratum to document cited in CA136:353395]

AUTHOR(S): Hodgson, Graeme.; Hager, Jeffrey H. H.; Volik, Stas.; Hariono, Sujatmi.; Wernick, Meredith.; Moore, Dan.; Nowak, Norma.; **Albertson, Donna G.**; **Pinkel, Daniel**; **Collins, Colin**; Hanahan, Douglas; **Gray, Joe W.**

CORPORATE SOURCE: Cancer Genetics and Breast Oncology Programs, UCSF Cancer Center, University of San Francisco at San Francisco, San Francisco, CA, 94143-0808, USA

SOURCE: Nature Genetics (2001), 29(4), 491
CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER: Nature America Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The name of the seventh author, Norma Nowak (Department of Human Genetics, Roswell Park **Cancer** Institute, Buffalo, new York 14263, USA), was omitted from the author list.

L32 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 2001:894920 CAPLUS

DOCUMENT NUMBER: 136:353395

TITLE: Genome scanning with array CGH delineates regional alterations in mouse islet **carcinomas**

AUTHOR(S): Hodgson, Graeme; Hager, Jeffrey H.; Volik, Stas; Hariono, Sujatmi; Wernick, Meredith; Moore, Dan; **Albertson, Donna G.**; Pinke, Daniel; **Collins, Colin**; Hanahan, Douglas; **Gray, Joe W.**

CORPORATE SOURCE: Cancer Genetics and Breast Onrology Programs, UCSF Cancer Center, University of California at San Francisco, San Francisco, CA, 94143-0808, USA

SOURCE: Nature Genetics (2001), 29(4), 459-464
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature America Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Carcinomas** that develop in the pancreatic islets of transgenic mice expressing the SV40 T-antigens (Tag) under transcriptional control of the rat insulin II promoter (RIP) progress through well-characterized stages that are similar to aspects of human **tumor** progression, including hyperplastic growth, increased angiogenesis and reduced apoptosis. The latter two stages have been associated with recurrent loss of heterozygosity (LOH) and reduced genome copy number on chromosomes 9 (LOH9) and 16 (LOH16), aberrations which we believe contribute to these phenotypes. Earlier analyses localized LOH9 to approx. 3 Mb and LOH16 to approx. 30 Mb (both syntenic with human 3q21-q25) but were limited by low throughput and a lack of informative polymorphic markers. Here we show that comparative genomic hybridization to DNA microarrays (array CGH) overcomes these limitations by allowing efficient, genome-wide analyses of relative genome copy number The CGH arrays used in these expts. carried BACs distributed at 2-20-MB intervals across the mouse genome and at higher d. in regions of interest. Using array CGH, we further narrowed the loci for LOH9 and LOH16 and defined new or previously unappreciated recurrent regions of copy-number decrease on chromosomes 6, 8 and 14 (syntenic with human chromosomes 12p11-p13. 16q24.3 and 13q11-q32, resp.) and regions of copy-number increase on chromosomes 2 and 4 (syntenic to human chromosomes 20q13.2 and 1p32-p36, resp.). Our analyses of human genome sequences syntenic to these regions suggest that **CYP24**, PFDN4, STMN1, CDKNIB, PPP2R3 and FSTL1 are candidate oncogenes or **tumor** -suppressor genes. We also show that irradiation and genetic background influence the spectrum of aberrations present in these **tumors**.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN

ACCESSION NUMBER: 2001:440426 BIOSIS
DOCUMENT NUMBER: PREV200100440426

TITLE: Genomic profiling of ovarian **cancer** by array comparative genomic hybridization.

AUTHOR(S): Kuo, Wen-Lin [Reprint author]; Polikoff, Daniel; Yamada, Kyosuke; Glenn, Pat; Zaloudek, Chuck; Smith-McCune, Karen; Mills, Gordon B.; Lu, Karen; Deavers, Mike; Shaw, Pat; **Collins, Colin**; Hamilton, Greg; Jain, Ajay; Brown, Nils; **Albertson, Donna**; **Pinkel, Dan**; **Gray, Joe W.**
CORPORATE SOURCE: MD Anderson Cancer Center, Houston, TX, USA

SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2001) Vol. 42, pp. 429. print.
Meeting Info.: 92nd Annual Meeting of the American Association for Cancer Research. New Orleans, LA, USA. March 24-28, 2001. American Association for Cancer Research.
ISSN: 0197-016X.
DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 19 Sep 2001
Last Updated on STN: 22 Feb 2002

L32 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2000:725793 CAPLUS
DOCUMENT NUMBER: 133:291918
TITLE: **CYP24** gene amplification and its use as marker for presence or progression of or predisposition to **cancer**
INVENTOR(S): **Albertson, Donna G.; Pinkel, Daniel ; Collins, Colin; Gray, Joe W.; Ystra, Bauke**
PATENT ASSIGNEE(S): Regents of the University of California, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000060109	A1	20001012	WO 2000-US5972	20000306
W: CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2367291	AA	20001012	CA 2000-2367291	20000306
EP 1255850	A1	20021113	EP 2000-916145	20000306
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY				

PRIORITY APPLN. INFO.: US 1999-285292 A 19990402
WO 2000-US5972 W 20000306

AB This invention pertains to the discovery that an amplification of the **CYP24** gene or an increase in **CYP24** activity is a marker for the presence of, progression of, or predisposition to, a **cancer** (e.g., breast **cancer**). Using this information, this invention provides methods of detecting a predisposition to **cancer** in an animal. The methods involve (i) providing a biol. sample from an animal (e.g. a human patient); (ii) detecting the level of **CYP24** within the biol. sample; and (iii) comparing the level of **CYP24** with a level of **CYP24** in a control sample taken from a normal, **cancer**-free tissue where an increased level of **CYP24** in the biol. sample compared to the level of **CYP24** in the control sample indicates the presence of said **cancer** in said animal.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 9 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2000:275749 BIOSIS
DOCUMENT NUMBER: PREV200000275749
TITLE: Identification of vitamin D 24 hydroxylase (**CYP24**) as a candidate oncogene by microarray CGH and

quantitative expression analysis.
AUTHOR(S): Ylstra, Bauke [Reprint author]; Livezey, Kristin W. [Reprint author]; **Albertson, Donna G.** [Reprint author]
CORPORATE SOURCE: UCSF Cancer Ctr, San Francisco, CA, USA
SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2000) No. 41, pp. 859. print.
Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 01-05, 2000.
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L32 ANSWER 10 OF 11 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2000296614 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10835626
TITLE: Quantitative mapping of amplicon structure by array CGH identifies **CYP24** as a candidate oncogene.
AUTHOR: **Albertson D G**; Ylstra B; Segraves R; **Collins C**; Dairkee S H; Kowbel D; Kuo W L; **Gray J W**; **Pinkel D**
CORPORATE SOURCE: [1] Cancer Research Institute, University of California, San Francisco, Box 0808, San Francisco, California, USA.. albertson@cc.ucsf.edu
CONTRACT NUMBER: CA45919 (NCI)
CA80314 (NCI)
HD17665 (NICHD)
+
SOURCE: Nature genetics, (2000 Jun) 25 (2) 144-6.
Journal code: 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000706
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AB We show here that quantitative measurement of DNA copy number across amplified regions using array comparative genomic hybridization (CGH) may facilitate oncogene identification by providing precise information on the locations of both amplicon boundaries and amplification maxima. Using this analytical capability, we resolved two regions of amplification within an approximately 2-Mb region of recurrent aberration at 20q13.2 in breast **cancer**. The putative oncogene ZNF217 (reference 5) mapped to one peak, and **CYP24** (encoding vitamin D 24 hydroxylase), whose overexpression is likely to lead to abrogation of growth control mediated by vitamin D, mapped to the other.

L32 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 1998:492622 CAPLUS
DOCUMENT NUMBER: 129:229013

TITLE: Positional cloning of ZNF217 and NABC1: genes amplified at 20q13.2 and overexpressed in breast **carcinoma**

AUTHOR(S): **Collins, Colin**; Rommens, Johanna M.; Kowbel, David; Godfrey, Tony; Tanner, Minna; Hwang, Soo-In; Polikoff, Daniel; Nonet, Genevieve; Cochran, Joanne; Myambo, Ken; Jay, Karen E.; Froula, Jeff; Cloutier, Thomas; Kuo, Wen-Lin; Yaswen, Paul; Dairkee, Shanaz; Giovanola, Jennifer; Hutchinson, Gordon B.; Isola, Jorma; Kallioniemi, Olli-P.; Palazzolo, Mike; Martin, Chris; Ericsson, Cheryl; **Pinkel, Dan**; **Albertson, Donna**; Li, Wu-Bo; **Gray, Joe W.**

CORPORATE SOURCE: Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA, 94720, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(15), 8703-8708
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors report here the mol. cloning of an ≈1-Mb region of recurrent amplification at 20q13.2 in breast **cancer** and other **tumors** and the delineation of a 260-kb common region of amplification. Anal. of the 1-Mb region produced evidence for five genes, ZNF217, ZNF218, and NABC1, PIC1L (PIC1-like), **CYP24**, and a pseudogene CRP (Cyclophillin Related Pseudogene). ZNF217 and NABC1 emerged as strong candidate oncogenes and were characterized in detail. NABC1 is predicted to encode a 585-aa protein of unknown function and is overexpressed in most but not all breast **cancer** cell lines in which it was amplified. ZNF217 is centrally located in the 260-kb common region of amplification, transcribed in multiple normal tissues, and overexpressed in all cell lines and **tumors** in which it is amplified and in two in which it is not. ZNF217 is predicted to encode alternately spliced, Kruppel-like transcription factors of 1,062 and 1,108 aa, each having a DNA-binding domain (eight C2H2 zinc fingers) and a proline-rich transcription activation domain.

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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